

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/628,126DATE: 10/05/2000  
TIME: 01:21:25

INPUT SET: S35970.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Goodwin, Raymond G.  
Smith, Craig A.  
Armitage, Richard J.  
Gruss, Hans-Jurgen

(ii) TITLE OF INVENTION: Novel Cytokine That Binds CD30

(iii) NUMBER OF SEQUENCES: 23

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
(B) STREET: 51 University Street  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98101

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Macintosh  
(C) OPERATING SYSTEM: Apple 7.1  
(D) SOFTWARE: Microsoft Word, Version 5.1a

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/628,126  
(B) FILING DATE: 28-JULY-2000  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/570,923  
(B) FILING DATE: 12-DEC-1995  
(A) APPLICATION NUMBER: US/08/225,989  
(B) FILING DATE: 12 APRIL 1994  
(A) APPLICATION NUMBER: US 07/966,775  
(B) FILING DATE: 27-OCT-1992  
(A) APPLICATION NUMBER: US 907,224  
(B) FILING DATE: 01-JUL-1992  
(A) APPLICATION NUMBER: US 899,660  
(B) FILING DATE: 15-JUN-1992  
(A) APPLICATION NUMBER: US 892,459  
(B) FILING DATE: 02-JUN-1992  
(A) APPLICATION NUMBER: US 889,717

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/628,126DATE: 10/05/2000  
TIME: 01:21:26

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47 (B) FILING DATE: 26-MAY-1992  
48  
49 (viii) ATTORNEY/AGENT INFORMATION:  
50 (A) NAME: Seese, Kathryn A.  
51 (B) REGISTRATION NUMBER: 32,172  
52 (C) REFERENCE/DOCKET NUMBER: 2804-E  
53  
54 (ix) TELECOMMUNICATION INFORMATION:  
55 (A) TELEPHONE: (206)587-0430  
56 (B) TELEFAX: (206)233-0644  
57 (C) TELEX: 756822  
58  
59  
60 (2) INFORMATION FOR SEQ ID NO:1:  
61  
62 (i) SEQUENCE CHARACTERISTICS:  
63 (A) LENGTH: 1788 base pairs  
64 (B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: single  
66 (D) TOPOLOGY: linear  
67  
68 (ii) MOLECULE TYPE: cDNA to mRNA  
69  
70 (iii) HYPOTHETICAL: NO  
71  
72 (iv) ANTI-SENSE: NO  
73  
74  
75 (vii) IMMEDIATE SOURCE:  
76 (B) CLONE: huCD30  
77  
78 (ix) FEATURE:  
79 (A) NAME/KEY: CDS  
80 (B) LOCATION: 1..1788  
81  
82  
83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
84  
85 ATG CGC GTC CTC CTC GCC GCG CTG GGA CTG CTG TTC CTG GGG GCG CTA 48  
86 Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu  
87 1 5 10 15  
88  
89 CGA GCC TTC CCA CAG GAT CGA CCC TTC GAG GAC ACC TGT CAT GGA AAC 96  
90 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn  
91 20 25 30  
92  
93 CCC AGC CAC TAC TAT GAC AAG GCT GTC AGG AGG TGC TGT TAC CGC TGC 144  
94 Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys  
95 35 40 45  
96  
97 CCC ATG GGG CTG TTC CCG ACA CAG CAG TGC CCA CAG AGG CCT ACT GAC 192  
98 Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp  
99 50 55 60

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100																			
101	TGC	AGG	AAG	CAG	TGT	GAG	CCT	GAC	TAC	TAC	CTG	GAT	GAG	GCC	GAC	CGC		240	
102	Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg			
103	65					70					75					80			
104																			
105	TGT	ACA	GCC	TGC	GTG	ACT	TGT	TCT	CGA	GAT	GAC	CTC	GTG	GAG	AAG	ACG		288	
106	Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr			
107					85					90					95				
108																			
109	CCG	TGT	GCA	TGG	AAC	TCC	TCC	CGT	GTC	TGC	GAA	TGT	CGA	CCC	GGC	ATG		336	
110	Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met			
111				100					105					110					
112																			
113	TTC	TGT	TCC	ACG	TCT	GCC	GTC	AAC	TCC	TGT	GCC	CGC	TGC	TTC	TTC	CAT		384	
114	Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His			
115			115					120					125						
116																			
117	TCT	GTC	TGT	CCG	GCA	GGG	ATG	ATT	GTC	AAG	TTC	CCA	GGC	ACG	GCG	CAG		432	
118	Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln			
119		130					135					140							
120																			
121	AAG	AAC	ACG	GTC	TGT	GAG	CCG	GCT	TCC	CCA	GGG	GTC	AGC	CCT	GCC	TGT		480	
122	Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys			
123	145					150					155					160			
124																			
125	GCC	AGC	CCA	GAG	AAC	TGC	AAG	GAA	CCC	TCC	AGT	GGC	ACC	ATC	CCC	CAG		528	
126	Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln			
127					165					170					175				
128																			
129	GCC	AAG	CCC	ACC	CCG	GTG	TCC	CCA	GCA	ACC	TCC	AGT	GCC	AGC	ACC	ATG		576	
130	Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met			
131				180					185					190					
132																			
133	CCT	GTA	AGA	GGG	GGC	ACC	CGC	CTC	GCC	CAG	GAA	GCT	GCT	TCT	AAA	CTG		624	
134	Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu			
135			195					200					205						
136																			
137	ACG	AGG	GCT	CCC	GAC	TCT	CCC	TCC	TCT	GTG	GGA	AGG	CCT	AGT	TCA	GAT		672	
138	Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser										

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153	TGT GCA TGG AAC TCC TCC CGC ACC TGC GAA TGT CGA CCT GGC ATG ATC	864
154	Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile	
155	275 280 285	
156		
157	TGT GCC ACA TCA GCC ACC AAC TCC TGT GCC CGC TGT GTC CCC TAC CCA	912
158	Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro	
159	290 295 300	
160		
161	ATC TGT GCA GGA GAG ACG GTC ACC AAG CCC CAG GAT ATG GCT GAG AAG	960
162	Ile Cys Ala Gly Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys	
163	305 310 315 320	
164		
165	GAC ACC ACC TTT GAG GCG CCA CCC CTG GGG ACC CAG CCG GAC TGC AAC	1008
166	Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn	
167	325 330 335	
168		
169	CCC ACC CCA GAG AAT GGC GAG GCG CCT GCC AGC ACC AGC CCC ACT CAG	1056
170	Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln	
171	340 345 350	
172		
173	AGC TTG CTG GTG GAC TCC CAG GCC AGT AAG ACG CTG CCC ATC CCA ACC	1104
174	Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr	
175	355 360 365	
176		
177	AGC GCT CCC GTC GCT CTC TCC TCC ACG GGG AAG CCC GTT CTG GAT GCA	1152
178	Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala	
179	370 375 380	
180		
181	GGG CCA GTG CTC TTC TGG GTG ATC CTG GTG TTG GTT GTG GTG GTC GGC	1200
182	Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Gly	
183	385 390 395 400	
184		
185	TCC AGC GCC TTC CTC CTG TGC CAC CGG AGG GCC TGC AGG AAG CGA ATT	1248
186	Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile	
187	405 410 415	
188		
189	CGG CAG AAG CTC CAC CTG TGC TAC CCG GTC CAG ACC TCC CAG CCC AAG	1296
190	Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys	
191	420 425 430	
192		
193	CTA GAG CTT GTG GAT TCC AGA CCC AGG AGG AGC TCA ACG CAG CTG AGG	1344
194	Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg	
195	435 440 445	
196		
197	AGT GGT GCG TCG GTG ACA GAA CCC GTC GCG GAA GAG CGA GGG TTA ATG	1392
198	Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met	
199	450 455 460	
200		
201	AGC CAG CCA CTG ATG GAG ACC TGC CAC AGC GTG GGG GCA GCC TAC CTG	1440
202	Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu	
203	465 470 475 480	
204		
205	GAG AGC CTG CCG CTG CAG GAT GCC AGC CCG GCC GGG GGC CCC TCG TCC	1488

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206  Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
207              485                      490                      495
208
209  CCC AGG GAC CTT CCT GAG CCC CGG GTG TCC ACG GAG CAC ACC AAT AAC 1536
210  Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
211              500                      505                      510
212
213  AAG ATT GAG AAA ATC TAC ATC ATG AAG GCT GAC ACC GTG ATC GTG GGG 1584
214  Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
215              515                      520                      525
216
217  ACC GTG AAG GCT GAG CTG CCG GAG GGC CGG GGC CTG GCG GGG CCA GCA 1632
218  Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
219              530                      535                      540
220
221  GAG CCC GAG TTG GAG GAG GAG CTG GAG GCG GAC CAT ACC CCC CAC TAC 1680
222  Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
223  545                      550                      555                      560
224
225  CCC GAG CAG GAG ACA GAA CCG CCT CTG GGC AGC TGC AGC GAT GTC ATG 1728
226  Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
227              565                      570                      575
228
229  CTC TCA GTG GAA GAG GAA GGG AAA GAA GAC CCC TTG CCC ACA GCT GCC 1776
230  Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
231              580                      585                      590
232
233  TCT GGA AAG TGA                                     1788
234  Ser Gly Lys
235              595
236
237
238  (2) INFORMATION FOR SEQ ID NO:2:
239
240      (i) SEQUENCE CHARACTERISTICS:
241          (A) LENGTH: 595 amino acids
242          (B) TYPE: amino acid
243          (D) TOPOLOGY: linear
244
245      (ii) MOLECULE TYPE: protein
246
247      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
248
249  Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
250      1              5              10              15
251

```

252 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn  
253 20 25 30  
254  
255 Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys  
256 35 40 45  
257  
258 Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/628,126**

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Line

Error

Original Text